

19. (Twice Amended) A method of identifying a compound that binds to a target RNA comprising:

generating *in silico* a virtual library of compounds predicted or calculated to interact with a molecular interaction site within said RNA;

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comparing three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing the highly ranked members of said hierarchy of compounds; and

testing said highly ranked members to determine their ability to interact with said molecular interaction site by:

contacting the target RNA with at least one of said highly ranked members to provide a complex between the RNA and the member or members;

ionizing said complex;

fragmenting the ionized complex; and

determining whether highly ranked members bind to the molecular interaction site of said RNA.

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21. (Twice Amended) A method of identifying a compound that binds to a target RNA comprising:

identifying at least one molecular interaction site on said target RNA, wherein said target RNA comprises single-stranded RNA and is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular

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interaction site.

26. (Amended) A method of identifying a compound that binds to a target RNA comprising:
identifying at least one molecular interaction site on said target RNA by comparing the nucleotide sequence of said target RNA with the nucleotide sequence of a RNA from a different taxonomic species, identifying at least one conserved region, determining the secondary structure of said conserved region;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

31. (Amended) A method of identifying a compound that binds to a target RNA comprising:
identifying at least one molecular interaction site on said target RNA by comparing the nucleotide sequence of said target RNA with the nucleotide sequence of RNA from a different taxonomic species, identifying at least one conserved region, and determining the secondary structure of said conserved region, wherein said target RNA comprises single-stranded RNA and is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

32. (Amended) A method of identifying a compound that binds to a target RNA comprising:
identifying at least one molecular interaction site on said target RNA

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing said highly ranked members of said hierarchy of compounds;

contacting said target RNA with at least one of said highly ranked members to provide a complex between said target RNA and said member or members;

ionizing said complex;

fragmenting said ionized complex; and

determining whether highly ranked member or members bind to said molecular interaction site of said RNA.

34. (Amended) A method of identifying a compound that binds to a target RNA comprising:
identifying at least one molecular interaction site on said target RNA, wherein said target RNA comprises single-stranded RNA and is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

synthesizing the highly ranked members of said hierarchy of compounds;

contacting said target RNA with at least one of said highly ranked members to provide a complex between said RNA and the member or members;

ionizing said complex;